IN THE SPECIFICATION:

Please **replace** Table 1, page 19 with the following Table 1:

Table 1

Name	Description	Sequence
ZElan144	PAX2 15 mer fragment-D form retroinversion	K(dns)-rtrlrrnhsshkant (SEQ ID NO:1)
ZElan145	P31 16 mer fragment- D form retroinversion	K(dns)-gphrrgrpnsrsskrt (SEQ ID NO:2)
ZElan146	HAX42 14 mer fragment-D form retroinversion	K(dns)-gtsngngccnydgp (SEQ ID NO:3)
ZElan129	PAX2 15 mer fragment	K(dns)-TNAKHSSHNRRLRTR (SEQ ID NO:4)
ZElan031	P31 16 mer fragment	K(dns)-TRKSSRSNPRGRRHPG (SEQ ID NO:5)
ZElan091	HAX42 14 mer fragment	K(dns)-PGDYNCCGNGNSTG (SEQ ID NO:6)

Please **replace** the paragraph at page 20, line 22 to page 21, line 2, with the following paragraph:

-- ZElan021, full length HAX42 [K(dns)-SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIPT] (SEQ ID NO:8) was given the arbitrary value of 1.00 for binding to P100 at a given peptide concentration determined from the signal-to-noise ratio data. Table 2 shows the results of P100 assays with the HAX42 related peptides ZElan021, Zelan091 and ZElan146. Assay number 1 was at 20 µg/ml; 2 and 3 were at 50 µg/ml; and 4 through 8 were at 25 µg/ml. The results for the retro-inverted form, Zelan 146 show reasonable binding compared to the HAX42 fragment Zelan091 and that the activity of the GIT targeting agent was not eliminated when converted to its retro-inverted form. --

Please **replace** the paragraph at page 21, lines 5-11 with the following paragraph:

--K_D values, or the concentration of the peptide required to reach half maximal binding to Caco-2 P100 fractions, are given in Table 3 for ZElan021, full length HAX42, [K(dns)-SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIPT] (SEQ ID NO:8), HAX42 fragment ZElan091, and the retro-inverted form of this fragment, ZElan146 as well as for ZElan018, full length PAX2, [K(dns)-STPPSREAYSRPYSVDS DSDTNAKHSSHNRRLRTRSRPNG] (SEQ ID NO:7), PAX2 fragment ZElan129, and the retro-inverted form of this fragment, ZELan144.--